

MOLECULAR EPIDEMIOLOGY OF *PSEUDOMONAS AERUGINOSA* AT A TERTIARY CARE HOSPITAL, SOUTHERN THAILAND

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Abstract. *Pseudomonas aeruginosa* ($n = 112$) isolates from various clinical specimens of hospitalized patients in Songklanagarind Hospital, southern Thailand from February 2012 to January 2013 were analyzed for susceptibility to 10 different antibiotics using a disk diffusion method and genetic relatedness by a pulsed-field gel electrophoretic (PFGE). Half of the strains were from sputum samples mainly of infected patients with cardiovascular disease. *P. aeruginosa* infection is significantly associated with age and length of hospital stay (p -value < 0.029). *P. aeruginosa* strains were equally sensitive (75-95%) to the four classes of antibiotics commonly used in Songklanagarind Hospital. Highest rate of resistance was to norfloxacin (43%) and no resistance to colistin was detected. Multidrug- and extensively drug-resistant *P. aeruginosa* (MDR-PA and XDR-PA) constituted 18% and 6%, respectively of the strains. PFGE DNA profiling revealed ≥ 70 relatedness among the strains, clustering into seven groups (A-G). The predominant group A and E (38 and 32% of typeable strains respectively) contained 21% of MDR-PA and 11% of XDR-PA strains. It was noticeable 40% of MDR and XDR-PA strains were from patients in intensive care unit and medical ward. In conclusion, the study shows the usefulness of PFGE DNA profiling in molecular epidemiological investigation of nosocomial *P. aeruginosa* infection allowing implementation of appropriate transmission control and prevention strategies.

Keywords: *Pseudomonas aeruginosa*, antibiogram, DNA profiling, molecular epidemiology, pulsed-field gel electrophoresis

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